

SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1) .. (18)

<223> rat NogoA_623-640

<400> 1

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Asp | Ser | Ile | Lys | Leu | Glu | Pro | Glu | Asn | Pro | Pro | Pro | Tyr | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Glu Ala

<210> 2

<211> 221

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1) .. (221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

<400> 2

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro
20 25 30

Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val

130

135

140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala
210 215 220

<210> 3

<211> 238

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1) .. (238)

<223> Light Chain of 11C7 with leader sequence

<400> 3

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile
20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu

115 120 125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys
225 230 235

<210> 4

<211> 3919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (3579)

<223> Human NogoA

<400> 4

atg gaa gac ctg gac cag tct cct ctg gtc tcg tcc tcg gac agc cca 48
Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
1 5 10 15

ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag 96
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30

gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc gcc ggg ctg tcc 192
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

gcg gcc cca gtg ccc acc gcc cct gcc gcc ggc gcg ccc ctg atg gac 240
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc 288
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala

| 85 | 90 | 95 | |
|---|-----|-----|-----|
| gct ccc ccc gtc gcc ccg gag cgg cag ccg tct tgg gac ccg agc ccg | | | 336 |
| Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro | | | |
| 100 | 105 | 110 | |
| gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc | | | 384 |
| Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val | | | |
| 115 | 120 | 125 | |
| tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc | | | 432 |
| Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro | | | |
| 130 | 135 | 140 | |
| cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc | | | 480 |
| Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr | | | |
| 145 | 150 | 155 | 160 |
| ccg cca gcc ccg gct ccc gcc gcg ccc ccc tcc acc ccg gcc gcg ccc | | | 528 |
| Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro | | | |
| 165 | 170 | 175 | |
| aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt | | | 576 |
| Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu | | | |
| 180 | 185 | 190 | |
| cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac | | | 624 |
| Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp | | | |
| 195 | 200 | 205 | |
| ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc | | | 672 |
| Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe | | | |
| 210 | 215 | 220 | |
| cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct | | | 720 |
| Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro | | | |
| 225 | 230 | 235 | 240 |

| | |
|---|------|
| ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca | 768 |
| Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser | |
| 245 250 255 | |
| aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct | 816 |
| Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala | |
| 260 265 270 | |
| tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat | 864 |
| Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp | |
| 275 280 285 | |
| tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc | 912 |
| Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe | |
| 290 295 300 | |
| agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg | 960 |
| Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg | |
| 305 310 315 320 | |
| gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt | 1008 |
| Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser | |
| 325 330 335 | |
| aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa | 1056 |
| Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys | |
| 340 345 350 | |
| ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt | 1104 |
| Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser | |
| 355 360 365 | |
| ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat | 1152 |
| Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr | |
| 370 375 380 | |

| | |
|--|------|
| gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag | 1200 |
| Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys | |
| 385 390 395 400 | |
| | |
| gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg | 1248 |
| Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu | |
| 405 410 415 | |
| | |
| gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act | 1296 |
| Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr | |
| 420 425 430 | |
| | |
| aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc | 1344 |
| Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro | |
| 435 440 445 | |
| | |
| agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt | 1392 |
| Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys | |
| 450 455 460 | |
| | |
| gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt | 1440 |
| Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe | |
| 465 470 475 480 | |
| | |
| cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa | 1488 |
| Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys | |
| 485 490 495 | |
| | |
| ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc | 1536 |
| Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr | |
| 500 505 510 | |
| | |
| aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat | 1584 |
| Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp | |
| 515 520 525 | |
| | |
| tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca | 1632 |

| | |
|---|------|
| Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala | |
| 530 535 540 | |
| aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa | 1680 |
| Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu | |
| 545 550 555 560 | |
| agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa | 1728 |
| Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys | |
| 565 570 575 | |
| atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct | 1776 |
| Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro | |
| 580 585 590 | |
| gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca | 1824 |
| Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser | |
| 595 600 605 | |
| cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt | 1872 |
| Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val | |
| 610 615 620 | |
| cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa | 1920 |
| Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu | |
| 625 630 635 640 | |
| gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc | 1968 |
| Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro | |
| 645 650 655 | |
| cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga | 2016 |
| Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly | |
| 660 665 670 | |
| ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa | 2064 |
| Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln | |

| | | | |
|---|-----|-----|------|
| 675 | 680 | 685 | |
| gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa | | | 2112 |
| Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu | | | |
| 690 | 695 | 700 | |
| aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa | | | 2160 |
| Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu | | | |
| 705 | 710 | 715 | 720 |
| atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa | | | 2208 |
| Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu | | | |
| 725 | 730 | 735 | |
| gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca | | | 2256 |
| Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser | | | |
| 740 | 745 | 750 | |
| ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa | | | 2304 |
| Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys | | | |
| 755 | 760 | 765 | |
| gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat | | | 2352 |
| Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn | | | |
| 770 | 775 | 780 | |
| aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg | | | 2400 |
| Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu | | | |
| 785 | 790 | 795 | 800 |
| gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct | | | 2448 |
| Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro | | | |
| 805 | 810 | 815 | |
| gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg | | | 2496 |
| Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met | | | |
| 820 | 825 | 830 | |

| | |
|---|------|
| gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct | 2544 |
| Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser | |
| 835 840 845 | |
| aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca | 2592 |
| Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro | |
| 850 855 860 | |
| att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat | 2640 |
| Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp | |
| 865 870 875 880 | |
| tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac | 2688 |
| Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His | |
| 885 890 895 | |
| aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc | 2736 |
| Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys | |
| 900 905 910 | |
| aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt | 2784 |
| Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val | |
| 915 920 925 | |
| gaa gag aaa atc agt ttc tca gat gac ttt tct aaa aat ggg tct gct | 2832 |
| Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala | |
| 930 935 940 | |
| aca tca aag gtg ctc tta ttg cct cca gat gtt tct gct ttg gcc act | 2880 |
| Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr | |
| 945 950 955 960 | |
| caa gca gag ata gag agc ata gtt aaa ccc aaa gtt ctt gtg aaa gaa | 2928 |
| Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu | |
| 965 970 975 | |

| | |
|---|------|
| gct gag aaa aaa ctt cct tcc gat aca gaa aaa gag gac aga tca cca | 2976 |
| Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro | |
| 980 985 990 | |
| tct gct ata ttt tca gca gag ctg agt aaa act tca gtt gtt gac ctc | 3024 |
| Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu | |
| 995 1000 1005 | |
| ctg tac tgg aga gac att aag aag act gga gtg gtg ttt ggt gcc | 3069 |
| Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala | |
| 1010 1015 1020 | |
| agc cta ttc ctg ctg ctt tca ttg aca gta ttc agc att gtg agc | 3114 |
| Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser | |
| 1025 1030 1035 | |
| gta aca gcc tac att gcc ttg gcc ctg ctc tct gtg acc atc agc | 3159 |
| Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser | |
| 1040 1045 1050 | |
| ttt agg ata tac aag ggt gtg atc caa gct atc cag aaa tca gat | 3204 |
| Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp | |
| 1055 1060 1065 | |
| gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa gtt gct ata | 3249 |
| Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile | |
| 1070 1075 1080 | |
| tct gag gag ttg gtt cag aag tac agt aat tct gct ctt ggt cat | 3294 |
| Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His | |
| 1085 1090 1095 | |
| gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt gat | 3339 |
| Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp | |
| 1100 1105 1110 | |
| gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt | 3384 |

| | |
|--|------|
| Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe | |
| 1115 1120 1125 | |
| acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg | 3429 |
| Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu | |
| 1130 1135 1140 | |
| gct ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat | 3474 |
| Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His | |
| 1145 1150 1155 | |
| cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt | 3519 |
| Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val | |
| 1160 1165 1170 | |
| aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag | 3564 |
| Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys | |
| 1175 1180 1185 | |
| cgc aaa gct gaa tga aaacgcccac aataattagt aggagttcat ctttaaaggg | 3619 |
| Arg Lys Ala Glu | |
| 1190 | |
| gatattcatt tgattatacy ggggaggggc agggaagaac gaaccttgac gttgcagtgc | 3679 |
| agtttcacag atcggttgta gatctttatt tttagccatg cactgttggtg aggaaaaatt | 3739 |
| acctgtcttg actgccatgt gttcatcatc ttaagtattg taagctgcta tgtatggatt | 3799 |
| taaaccgtaa tcatatcttt ttcctatctg aggcactggt ggaataaaaa acctgtatat | 3859 |
| tttactttgt tgcagatagt cttgccgcat cttggcaagt tgcagagatg gtggagctag | 3919 |

<211> 1192

<212> PRT

<213> Homo sapiens

<400> 5

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro
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Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
20 25 30

Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
115 120 125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
130 135 140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145 150 155 160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
165 170 175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu
180 185 190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp
195 200 205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe
210 215 220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro
225 230 235 240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser
245 250 255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp
275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe
290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg
305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser
325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys
340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser
355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys
385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu

| | | |
|---|-----|-----|
| 405 | 410 | 415 |
| Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr | | |
| 420 | 425 | 430 |
| Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro | | |
| 435 | 440 | 445 |
| Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys | | |
| 450 | 455 | 460 |
| Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe | | |
| 465 | 470 | 475 |
| 480 | | |
| Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys | | |
| 485 | 490 | 495 |
| Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr | | |
| 500 | 505 | 510 |
| Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp | | |
| 515 | 520 | 525 |
| Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala | | |
| 530 | 535 | 540 |
| Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu | | |
| 545 | 550 | 555 |
| 560 | | |

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys
565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn
770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu

| 995 | 1000 | 1005 |
|-----------------------------|---------------------|-------------|
| Leu Tyr Trp Arg Asp Ile Lys | Lys Thr Gly Val Val | Phe Gly Ala |
| 1010 | 1015 | 1020 |
| Ser Leu Phe Leu Leu Leu Ser | Leu Thr Val Phe Ser | Ile Val Ser |
| 1025 | 1030 | 1035 |
| Val Thr Ala Tyr Ile Ala Leu | Ala Leu Leu Ser Val | Thr Ile Ser |
| 1040 | 1045 | 1050 |
| Phe Arg Ile Tyr Lys Gly Val | Ile Gln Ala Ile Gln | Lys Ser Asp |
| 1055 | 1060 | 1065 |
| Glu Gly His Pro Phe Arg Ala | Tyr Leu Glu Ser Glu | Val Ala Ile |
| 1070 | 1075 | 1080 |
| Ser Glu Glu Leu Val Gln Lys | Tyr Ser Asn Ser Ala | Leu Gly His |
| 1085 | 1090 | 1095 |
| Val Asn Cys Thr Ile Lys Glu | Leu Arg Arg Leu Phe | Leu Val Asp |
| 1100 | 1105 | 1110 |
| Asp Leu Val Asp Ser Leu Lys | Phe Ala Val Leu Met | Trp Val Phe |
| 1115 | 1120 | 1125 |
| Thr Tyr Val Gly Ala Leu Phe | Asn Gly Leu Thr Leu | Leu Ile Leu |
| 1130 | 1135 | 1140 |

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys
1175 1180 1185

Arg Lys Ala Glu
1190

<210> 6

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (18)

<223> Human NogoA_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1 5 10 15

Glu Ala

<210> 7

<211> 819

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(819)

<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg
1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile
20 25 30

Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val

305 310 315 320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp
355 360 365

Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr
370 375 380

Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val
385 390 395 400

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu
405 410 415

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu
420 425 430

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln
435 440 445

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile
450 455 460

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn
610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys
625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser
645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu
660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr
675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr
690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp
705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu
725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser
805 810 815

Lys Thr Ser

<210> 8

<211> 10

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (10)

<223> hypervariable part of heavy chain of 11C7

<400> 8

Gly Phe Asp Phe Arg Arg Asn Trp Met Ser
1 5 10

<210> 9

<211> 17

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(17)

<223> hypervariable part of heavy chain of 11C7

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys
1 5 10 15

Asp

<210> 10

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of heavy chain of 11C7

<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr

1

5

<210> 11

<211> 16

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (16)

<223> hypervariable part of light chain of 11C7

<400> 11

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ser | Ser | Gln | Ser | Leu | Leu | His | Ser | Asp | Gly | Lys | Thr | Tyr | Leu | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser

1 5

<210> 13

<211> 9

<212> PRT

<213> Mus musculus

<220>

<221> BINDING

<222> (1) .. (9)

<223> hypervariable part of light chain of 11C7

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr

1 5

<210> 14

<211> 30

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (30)

<223> DNA-CDR1-11C7

<400> 14

ggattcgatt ttagaagaaa ttggatgagt

30

<210> 15

<211> 51

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (51)

<223> DNA-CDR2-11C7

<400> 15

gaaattaatc cagatagcag taagataaac tatacgccat ctctaaagga t 51

<210> 16

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (27)

<223> DNA-CDR3-11C7

<400> 16

ccggtctgga tgtatgctat ggactac 27

<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (48)

<223> DNA-CDR'1-11C7

<400> 17

aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat

48

<210> 18

<211> 21

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (21)

<223> DNA-CDR'2-11C7

<400> 18

ctgggtgtcta aactggactc t

21

<210> 19

<211> 27

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (27)

<223> DNA-CDR'3-11C7

<400> 19

tggcaaggta cacattttcc tcagacg

27

<210> 20

<211> 54

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(54)

<223> leader sequence for heavy chain of 11C7

<400> 20

atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val

1 5 10 15

cag tgt 54

Gln Cys

<210> 21

<211> 18

<212> PRT

<213> Mus musculus

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val
1 5 10 15

Gln Cys

<210> 22

<211> 57

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(57)

<223> leader sequence for 11C7-light chain

<400> 22

atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

acc agc ggt
Thr Ser Gly

57

<210> 23

<211> 19

<212> PRT

<213> Mus musculus

<400> 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu
1 5 10 15

Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) .. (181)

<223> human Nig-D20

<400> 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser
1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile

115

120

125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro

130

135

140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro

145

150

155

160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu

165

170

175

Pro Val Asp Leu Phe

180

<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1) .. (3492)

<223> rat NogoA

<400> 25

atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc acg gac agc 48
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc . 96
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro .
20 25 30

gag gac gag gag gac gag gag gag gag gag gac gag gag gag gac gac 144
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac 240
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc 288
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

gag ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc 336
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc ctg ccc tcc 384
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

| | |
|---|-----|
| aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg cct ccg ccg | 432 |
| Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro | |
| 130 135 140 | |
| cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc cct tcc acg | 480 |
| Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr | |
| 145 150 155 160 | |
| ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat gag acc ctt | 528 |
| Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu | |
| 165 170 175 | |
| ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa | 576 |
| Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu | |
| 180 185 190 | |
| aaa att atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt | 624 |
| Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly | |
| 195 200 205 | |
| caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct | 672 |
| Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro | |
| 210 215 220 | |
| tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat gga tac ctt | 720 |
| Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu | |
| 225 230 235 240 | |
| ggt aac tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act | 768 |
| Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr | |
| 245 250 255 | |
| tta aat gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt | 816 |
| Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe | |
| 260 265 270 | |
| gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg | 864 |

| | |
|---|------|
| Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met | |
| 275 280 285 | |
| gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta | 912 |
| Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val | |
| 290 295 300 | |
| gaa aac act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat | 960 |
| Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp | |
| 305 310 315 320 | |
| tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt | 1008 |
| Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly | |
| 325 330 335 | |
| aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat | 1056 |
| Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn | |
| 340 345 350 | |
| gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac | 1104 |
| Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp | |
| 355 360 365 | |
| ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga | 1152 |
| Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly | |
| 370 375 380 | |
| agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac | 1200 |
| Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp | |
| 385 390 395 400 | |
| aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat | 1248 |
| Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp | |
| 405 410 415 | |
| agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct | 1296 |
| Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro | |

| | | | |
|---|-----|-----|------|
| 420 | 425 | 430 | |
| gtg aag gac agc tcc aga gca tat att acc tgt gct tcc ttt acc tca | | | 1344 |
| Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser | | | |
| 435 | 440 | 445 | |
| gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat | | | 1392 |
| Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His | | | |
| 450 | 455 | 460 | |
| act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc | | | 1440 |
| Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala | | | |
| 465 | 470 | 475 | 480 |
| caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt | | | 1488 |
| Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu | | | |
| 485 | 490 | 495 | |
| gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta | | | 1536 |
| Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu | | | |
| 500 | 505 | 510 | |
| tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg | | | 1584 |
| Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr | | | |
| 515 | 520 | 525 | |
| cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca | | | 1632 |
| Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr | | | |
| 530 | 535 | 540 | |
| ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca | | | 1680 |
| Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser | | | |
| 545 | 550 | 555 | 560 |
| gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca | | | 1728 |
| Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser | | | |
| 565 | 570 | 575 | |

| | |
|---|------|
| ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt | 1776 |
| Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val | |
| 580 585 590 | |
| atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta | 1824 |
| Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val | |
| 595 600 605 | |
| gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat | 1872 |
| Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr | |
| 610 615 620 | |
| gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc | 1920 |
| Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala | |
| 625 630 635 640 | |
| atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag | 1968 |
| Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu | |
| 645 650 655 | |
| cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata | 2016 |
| Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile | |
| 660 665 670 | |
| tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca | 2064 |
| Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro | |
| 675 680 685 | |
| agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg | 2112 |
| Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser | |
| 690 695 700 | |
| gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa | 2160 |
| Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu | |
| 705 710 715 720 | |

| | |
|---|------|
| cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca | 2208 |
| Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr | |
| 725 730 735 | |
| caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct | 2256 |
| Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser | |
| 740 745 750 | |
| gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag | 2304 |
| Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln | |
| 755 760 765 | |
| gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt | 2352 |
| Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser | |
| 770 775 780 | |
| aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag | 2400 |
| Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu | |
| 785 790 795 800 | |
| aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat | 2448 |
| Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn | |
| 805 810 815 | |
| gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca | 2496 |
| Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr | |
| 820 825 830 | |
| ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt | 2544 |
| Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe | |
| 835 840 845 | |
| gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat | 2592 |
| Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp | |
| 850 855 860 | |
| cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca | 2640 |

| | | | |
|---------|---------------------|---------------------|------------------|
| 1010 | 1015 | 1020 | |
| agc ttt | agg ata tat aag ggc | gtg atc cag gct atc | cag aaa tca 3114 |
| Ser Phe | Arg Ile Tyr Lys Gly | Val Ile Gln Ala Ile | Gln Lys Ser |
| 1025 | 1030 | 1035 | |
| gat gaa | ggc cac cca ttc agg | gca tat tta gaa tct | gaa gtt gct 3159 |
| Asp Glu | Gly His Pro Phe Arg | Ala Tyr Leu Glu Ser | Glu Val Ala |
| 1040 | 1045 | 1050 | |
| ata tca | gag gaa ttg gtt cag | aaa tac agt aat tct | gct ctt ggt 3204 |
| Ile Ser | Glu Glu Leu Val Gln | Lys Tyr Ser Asn Ser | Ala Leu Gly |
| 1055 | 1060 | 1065 | |
| cat gtg | aac agc aca ata aaa | gaa ctg agg cgg ctt | ttc tta gtt 3249 |
| His Val | Asn Ser Thr Ile Lys | Glu Leu Arg Arg Leu | Phe Leu Val |
| 1070 | 1075 | 1080 | |
| gat gat | tta gtt gat tcc ctg | aag ttt gca gtg ttg | atg tgg gtg 3294 |
| Asp Asp | Leu Val Asp Ser Leu | Lys Phe Ala Val Leu | Met Trp Val |
| 1085 | 1090 | 1095 | |
| ttt act | tat gtt ggt gcc ttg | ttc aat ggt ctg aca | cta ctg att 3339 |
| Phe Thr | Tyr Val Gly Ala Leu | Phe Asn Gly Leu Thr | Leu Leu Ile |
| 1100 | 1105 | 1110 | |
| tta gct | ctg atc tca ctc ttc | agt att cct gtt att | tat gaa cgg 3384 |
| Leu Ala | Leu Ile Ser Leu Phe | Ser Ile Pro Val Ile | Tyr Glu Arg |
| 1115 | 1120 | 1125 | |
| cat cag | gtg cag ata gat cat | tat cta gga ctt gca | aac aag agt 3429 |
| His Gln | Val Gln Ile Asp His | Tyr Leu Gly Leu Ala | Asn Lys Ser |
| 1130 | 1135 | 1140 | |
| gtt aag | gat gcc atg gcc aaa | atc caa gca aaa atc | cct gga ttg 3474 |
| Val Lys | Asp Ala Met Ala Lys | Ile Gln Ala Lys Ile | Pro Gly Leu |
| 1145 | 1150 | 1155 | |

aag cgc aaa gca gat tga

3492

Lys Arg Lys Ala Asp

1160

<210> 26

<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
1 5 10 15

Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro

675

680

685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser

690

695

700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu

705

710

715

720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr

725

730

735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser

740

745

750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln

755

760

765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser

770

775

780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu

785

790

795

800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn

805

810

815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
835 840 845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val
 1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile
 1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu
1145 1150 1155

Lys Arg Lys Ala Asp
1160

<210> 27

<211> 25

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1) .. (25)

<223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1) .. (17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer_bind

<222> (1) .. (25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer_bind

<222> (1) .. (28)

<223>

<400> 30

aactgcagta ctgagctcct ccattctgc

28

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'

<220>

<221> primer_bind

<222> (1) .. (33)

<223> forward primer

<400> 31

gtcgcggatc catggagacc ctttttgetc ttc

33

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'

<220>

<221> primer_bind

<222> (1) .. (27)

<223> reverse primer

<400> 32

gttctcgagt tatgaagttt tactcag

.27

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'-1

<220>

<221> primer_bind

<222> (1) .. (29)

<223> primer

<400> 33

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29

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 34

gtttctcgag tgaagtttta ttcagctc

28

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer

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<221> primer_bind

<222> (1) .. (20)

<223> primer

<400> 35

tccaccccg g ccgcgccaa

20

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer 2

<220>

<221> primer_bind

<222> (1) .. (22)

<223> primer

<400> 36

aatgatgggc aaagctgtgc tg

22

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer_bind

<222> (1) .. (24)

<223> primer

<400> 37

ggtacaaaga ttgcttatga aaca

24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer_bind

<222> (1) .. (22)

<223> primer

<400> 38

agcagggcca aggcaatgta gg

22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VL leader

<220>

<221> primer_bind

<222> (1)..(28)

<223> primer

<400> 39

aatatgagtc ctgcccagtt cctgtttc

28

<210> 40

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-Ck

<220>

<221> primer_bind

<222> (1) .. (32)

<223> primer

<400> 40

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32

<210> 41

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VH leader

<220>

...

<222> (1) .. (31)

<223> primer

<400> 41

aatatggatt ttgggctgat tttttttatt g

31

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-CH hinge

<220>

<221> primer_bind

<222> (1) .. (24)

<223> primer

<400> 42

aattgggcaa cgttgcaggt gacg

24

<210> 43

<211> 663

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1)..(663)

<223> DNA variable part of heavy chain 11C7

<400> 43

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| aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt | 120 |
| gtagtctcag gattcgattt tagaagaaat tggatgagtt ggggccggca ggctcctggg | 180 |
| aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca | 240 |
| tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgct gtacctgcaa | 300 |
| gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg | 360 |
| tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca | 420 |
| cccccatctg tctatccact ggcccctgga tctgctgccc aaactaactc catggtgacc | 480 |

ctgggatgcc tgggtcaaggg ctatttcctt gagccagtga cagtgacctg gaactctgga 540
tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgacct ctacactctg 600
agcagctcag tgactgtccc ctccagcacc tggcccagcg agaccgtcac ctgcaacgtt 660
gcc 663

<210> 44

<211> 717

<212> DNA

<213> Mus musculus

<220>

<221> misc_binding

<222> (1) .. (717)

<223> variable part of light chain of 11C7

<400> 44

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gttctgttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc 120
tcttgcaagt caagtcagag cctcttgcac agtgcgtgga agacatattt gaattgggtg 180

| | |
|---|-----|
| ttacagaggc caggccagtc tccaaagcgc ctaatctatc tgggtgtctaa actggactct | 240 |
| ggagtcacctg acagggttcac tggcagtgga tcagggacgg atttcacact gaaaatcagc | 300 |
| agagtggagg ctgaggattt gggactttat tattgctggc aaggtaacaca ttttcctcag | 360 |
| acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc | 420 |
| atcttccac catccagtga gcagttaaca tctggaggtg cctcagtcgt gtgcttcttg | 480 |
| aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa | 540 |
| aatggcgctc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc | 600 |
| agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc | 660 |
| actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag | 717 |